IN THE UNITED STATES DISTRICT COURT
FOR THE DISTRICT OF DELAWARE

INVITAE CORPORATION,	)	
	)	
Plaintiff,	)	
	)	
v.	)	C.A. No. 21-669 (LPS)
	)	
NATERA, INC.,	)	
	)	
Defendant.	)	

NATERA, INC.'S OPENING BRIEF IN SUPPORT OF ITS MOTION TO DISMISS PURSUANT TO RULE 12(b)(6) FOR LACK OF PATENTABLE SUBJECT MATTER

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I. NATURE AND STAGE OF THE PROCEEDINGS

Invitae Corporation's Complaint alleges infringement of U.S. Patent No. 10,604,799 (the "'799 patent"). D.I. 1; D.I. 1-1, Ex. 1. Natera moves to dismiss the Complaint under Fed. R. Civ. P. 12(b)(6) for failure to state a claim of patent infringement upon which relief could be granted because the claims of the '799 patent are drawn to patent ineligible subject matter.

II. SUMMARY OF THE ARGUMENT

The '799 patent claims an abstract idea: an algorithmic method of manipulating and combining genetic sequence data using an intermediate data set. *See* D.I. 1-1, Ex. 1 at cl. 1.[1] The patent suggests that combining raw sequence data ("sequence reads") to yield an intermediate "contig" to facilitate comparison to a reference sequence is better than directly comparing individual sequence reads to the reference. But even alleged "improved" abstract ideas are still abstract ideas and remain unpatentable without significantly more.

Nothing significantly more is claimed here. The claims do not recite an inventive concept. Aside from the abstract idea itself, the patent admits that every other feature of the claimed methods was well understood, routine, and conventional. The claims specify using a generic computer for the data manipulation, and the law is well established that such "do it on a computer" claims do not pass muster under 35 U.S.C. § 101.[2] Because no re-pleading can cure these deficiencies, the Complaint should therefore be dismissed with prejudice.

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[1] Invitae alleges that claim 1 is representative. D.I. 1 at ¶ 15. Natera consents to claim 1 of the '799 patent as representative for the purposes of this motion.

[2] As the Federal Circuit has held, "it is not enough, however, to merely improve a fundamental practice or abstract process by invoking a computer merely as a tool." *Affinity Labs. of Texas, LLC v. DIRECTV, LLC*, 838 F.3d 1253, 1258 (Fed. Cir. 2016).

III. STATEMENT OF FACTS

A. DNA Sequencing and Data Processing

DNA sequencing is the process of determining the order of nucleotides (As, Ts, Cs, or Gs) of DNA in a sample. DNA fragments may be sequenced using a commercial sequencing machine and the resulting sequence data are stored in a computer as "sequence reads."

Sequence reads can be arranged by a computer into longer "contigs" by examining how they overlap. For example, overlapping sequence reads can be joined, like links in a chain, to produce a contig sequence containing the very same sequence data as the overlapping reads. *Id.* at 12:65-66. The '799 patent explains that contigs were known in the art, and that numerous prior art algorithms can be used to generate them. *Id.* at 13:25-16:29. The patent does not purport to provide any new way of assembling contigs.

A "reference genome," such as the human genome, is a digital nucleic acid sequence database representing the genes in an idealized individual organism (such as human). *Id.* at 1:38-40. Sample DNA sequences can be aligned and compared to a reference genome to find differences (or "variants"), such as mutations, and their positional information relative to the reference. The '799 patent explains that numerous prior art computer programs can be used to align DNA sequences and find information about mutations. *Id.* at 19:11-20:21.

B. What Is Claimed: An Algorithmic Method of Manipulating and Combining Data Using an Intermediate Data Set

Entitled "Sequence Assembly," the '799 patent claims a method for assembling DNA sequence reads using a generic computer. Claim 1, the only independent claim, states:

1. A method for assembling sequence reads, the method comprising:

obtaining a sample comprising template nucleic acid;

sequencing the template nucleic acid to generate a plurality of sequence reads;

> *inputting* a reference genome and said plurality of sequence reads into a computer system comprising a processor coupled to a non-transitory memory to perform the steps of:
>
> > *assembling* a contig from at least some of the plurality of sequence reads;
> >
> > identifying a plurality of contig:reference descriptions of mutations by *aligning* the contig to said reference genome;
> >
> > identifying a plurality of read:contig descriptions by *aligning* each of the plurality of sequence reads to the contig; and
> >
> > *combining* the contig:reference descriptions with the read:contig descriptions to produce read:reference descriptions to map positional information of mutations found in the individual reads relative to the reference.

Id. at cl. 1 (discrete steps italicized).

Obtaining: The first step is to obtain a biological sample containing the "template nucleic acid" to be analyzed. As the patent acknowledges, the sample may be obtained "by a variety of techniques" known in the literature, *id.* at 6:30-36.

Sequencing: The prior art taught the sequencing techniques recited in the claims, and the '799 patent offers nothing more. *See generally* D.I. 1-1, Ex. 1 at 9:56-12:23. The patent explains that sequencing can be done using commercially available sequencing machines or "any method known in the art." *Id.* at 9:56-12:23. The sequencing machine generates short "reads" representing the sequences of the DNA fragments. *Id.* at 12:25-26. From this point onward, the method is concerned with digitized genetic data, not the physical, chemical elements of DNA.

Inputting: The "sequence read" data is then inputted into a computer, along with the sequence of "a reference genome." *See id.* at FIG. 1 (step 101).

Assembling: At this step, the computer assembles the sequence reads into a "contig"—a longer, contiguous sequence—based on overlapping regions in the reads. *Id.* at 13:4-24; FIG. 1 (step 105); FIG. 2 (step 1). The patent admits that this was nothing new: "Reads can be assembled into contigs by any method known in the art." *Id.* at 13:25-26. These methods are algorithms that

compare reads to find the overlaps based on mathematical calculations of the probabilities of various arrangements, and the patent lists numerous preexisting methods. *Id.* at 13:25-16:27.

Contig:Genome Alignment: Next, the computer identifies a set of descriptions of mutations by aligning the assembled contig with the reference genome, *i.e.*, algorithmically positioning the contig along the reference genome. *Id.* at 16:54-55; FIG. 1 (steps 109, 113); FIG. 2 (step 2). As with contig assembly, this is fundamentally a probabilistic process, and, too, can be performed "using any suitable computer program known in the art." *Id.* at 19:11-13. "With each contig aligned to the reference genome, any differences between the contig and the reference genome can be identified by a comparison." *Id.* at 20:22-24. Differences between the contig and the reference genome are deemed "mutations," described in the assembly algorithm as a "contig:reference description of mutation." *Id.* at 20:35-39.

Read:Contig Alignment: The computer next identifies another set of descriptions of mutations by aligning each of the sequence reads to the contig itself and describes each read with reference to the contig, referred to as a "read:contig description." *Id.* at 21:5-8; FIG. 1 (step 117); FIG. 2 (step 3).

Combining: The final step in claim 1 is to combine the two sets of data—the "contig:reference description of mutation" and the "read:contig description"—to obtain a "read:reference description." *Id.* at 21:18-21; FIG. 2 (step 4). "This combination gives, for any mutation detected in the nucleic acid, a description of that mutation by reference to the reference genome." *Id.* at 21:22-24. Once combined, "positional and variant information" of a mutation in a raw sequence read can be mapped to the reference genome. *Id.* at 2:48-49.

The dependent claims add limitations that specify certain characteristics of the data processed by the algorithm (*i.e.*, dictate how the sequence reads are obtained using prior art

techniques) or require certain algorithmic manipulations, which are themselves abstract. None of these alter the fundamental nature of the claims.

IV. LEGAL STANDARD

Where, as here, there are no facts in dispute, the Court may resolve a Section 101 challenge on a motion to dismiss. *See Aatrix Software, Inc. v. Green Shades Software, Inc.*, 882 F.3d 1121, 1125 (Fed. Cir. 2018); *Berkheimer v. HP Inc.*, 881 F.3d 1360, 1368 (Fed. Cir. 2018); *see also Citrix Sys., Inc. v. Avi Networks, Inc.*, 363 F. Supp. 3d 511, 520 (D. Del. 2019); *Search & Soc. Media Partners, LLC v. Facebook, Inc.*, 346 F. Supp. 3d 626, 633 (D. Del. 2018). The Court may base its decision on the patent itself as well as the well pleaded allegations of the Complaint. *See Genetic Techs. Ltd. v. Bristol-Myers Squibb Co.*, 72 F. Supp. 3d 521, 526 (D. Del. 2014), *aff'd sub nom. Genetic Techs. Ltd. v. Merial L.L.C.*, 818 F.3d 1369 (Fed. Cir. 2016). The Court need not accept a plaintiff's conclusory allegations or legal assertions as true. *See Ashcroft v. Iqbal*, 556 U.S. 662, 678 (2009); *Bell Atlantic Corp. v. Twombly*, 550 U.S. 544, 556 (2007); *Morrow v. Balaski*, 719 F.3d 160, 165 (3d Cir. 2013).

The two-step patent-eligibility analysis of *Alice* governs. *See Alice Corp. Pty. v. CLS Bank Int'l*, 573 U.S. 208, 217-18 (2014). Step one asks whether the patent claims are directed to an ineligible subject matter—here, an "abstract idea." *See id.* at 217. If the claims are drawn to an abstract idea, then at step two the court determines whether the claims include an "inventive concept sufficient to transform the claimed abstract idea into a patent-eligible application." *Id.* Where the "additional features" recite nothing more than "well-understood, routine, conventional activity," the abstract idea is patent ineligible. *Intellectual Ventures I LLC v. Erie Indemnity Co.*, 850 F.3d 1315, 1328 (Fed Cir. 2017).

V. THE '799 PATENT IS INELIGIBLE UNDER SECTION 101

All of Invitae's allegations relating to patent eligibility under Section 101 are found in six paragraphs: Paragraphs 13-14 allege the problems the purported invention address (citing three passages from the patent); paragraph 15 alleges the claims are "directed to" a technique for improving DNA technology (citing claim 1); paragraph 16 appears to allege a technological improvement (citing claim 1); paragraph 17 alleges the steps of the claims are "not routine and conventional" (appearing to cite claim 1); and paragraph 18 alleges the claims encompass an inventive concept (citing two passages from the patent). As discussed below, the patent and Invitae's allegations confirm that the '799 patent claims are directed to an abstract idea, and there is no inventive concept in the claims that would satisfy Section 101.

A. *Alice* Step One: The '799 Patent Is Directed to the Abstract Idea of Manipulating and Combining Data

1. *The '799 patent claims are analogous to data manipulation and processing claims the Federal Circuit has found to be directed to abstract ideas*

The '799 patent claims are directed to an algorithmic method of manipulating and combining genetic sequence data using an intermediate data set. As illustrated by claim 1 above, the patent claims a process where genetic sequence data are algorithmically assembled, aligned, and combined. The written description also makes clear that the focus of the claimed invention is on the mathematical operation of assembling, aligning, and combining genetic sequence data.

According to the '799 patent, existing methods lack "positional accuracy" and "do a poor job of correctly interpreting certain mutations[.]" D.I. 1-1, Ex. 1 at 2:21-26. The claimed invention supposedly solves this problem by making use of an intermediate data set, called a "contig," and "combin[ing] a contig based sequencing assembly approach with an individual alignment based sequence assembly approach":

SUMMARY

> The invention generally relates to genotyping nucleic acids through methods of assembling and aligning sequence reads. Methods of the invention ***combine a contig based sequence assembly approach with an individual alignment based sequence assembly approach in order to more accurately assemble sequence reads***. Methods of the invention are accomplished by assembling contigs from sequence reads, aligning the contigs to a reference sequence, aligning the reads back to the contig, and identifying mutations via the assembled contig and the alignments.

D.I. 1-1, Ex. 1 at 2:30-39 (emphasis added); *see also id.* at FIGS. 1-3 (illustrating methods of invention). "***By combining information in this way***, the limitations of a tradeoff between substitution sensitivity and deletion sensitivity is overcome." *Id.* at 4:52-54 (emphasis added).

To determine whether claims are "directed to" an abstract idea, courts "compare the claims at issue to those claims already found to be directed to an abstract idea in previous cases." *In-Depth Test, LLC v. Maxim Integrated, Prods., Inc.*, C.A. Nos. 14-887-CFC, 14-888-CFC, 2018 WL 6617142 at *4 (D. Del. Dec. 18, 2018) (citing *Enfish, LLC v. Microsoft Corp.*, 822 F.3d 1327, 1334 (Fed. Cir. 2016)).

Here, the '799 patent claims are highly analogous to those the Federal Circuit found to be directed to an abstract idea in *In re Stanford*, where the claims were drawn to a "computerized method of inferring haplotype phase in a collection of unrelated individuals." 991 F.3d 1245, 1250-51 (Fed. Cir. 2021). Like the claims of the '799 patent, the claims at issue in *Stanford* started and ended with genetic data, were focused on "the use of mathematical calculations and statistical modeling" to manipulate genetic data (haplotype phase), and were not drawn to any "practical, technological improvements extending beyond improving the accuracy of a mathematically calculated statistical prediction." *Id.* "The different use of a mathematical calculation, even one that yields different or better results, does not render patent eligible subject matter." *Id.* at 1251.

While *Stanford* is particularly analogous to the '799 claims given its application of algorithms to genetic data, the Federal Circuit routinely finds claims in other application contexts that are drawn to combining data into a new form without tangible transformation to be directed to an abstract idea. For example, in *Digitech*, the Federal Circuit held that a claim reciting "***taking two data sets and combining them into a single data set***" was directed to an abstract idea because the data sets were drawn from "existing information" and simply organized "into a new form." *Digitech Image Techs., LLC v. Elecs. for Imaging, Inc.*, 758 F.3d 1344, 1351 (Fed. Cir. 2014) (emphasis added). Here, the '799 patent claims recite the use of two data sets (the "contig:ref" and "read:contig" data sets) which are combined into a single data set (the "read:reference" data set). In *RecogniCorp*, claims that recited "a process that started with data, added an algorithm, and ended with a new form of data" were found to be directed to an abstract idea. *RecogniCorp, LLC v. Nintendo Co.*, 855 F.3d 1322, 1327 (Fed. Cir. 2017). Again, the claims at issue here merely recite applying known algorithms to two data sets in order to obtain a new form of that same data. *See also Berkheimer*, 881 F.3d at 1366 (claims "directed to the abstract idea of parsing, comparing, storing, and editing data"); *Elec. Power Group, LLC v. Alstom S.A.*, 830 F.3d 1350, 1353 (Fed. Cir. 2016) (claims focused on "collecting information, analyzing it, and displaying certain results of the collection and analysis" directed to an abstract idea).

Indeed, the data manipulation and comparison claimed in the '799 patent could just as easily be performed on any sequence of 1s and 0s or any other sequence of letters and numbers, and the Federal Circuit has confirmed that comparing genetic codes, without more, is just as abstract as comparing binary codes. *See In re BRCA1- & BRCA2-Based Hereditary Cancer Test Patent Litig.*, 774 F.3d 755, 763 (Fed. Cir. 2014).

2. *No technological improvement offered by the '799 patent claims*

As the above cases show, it does not matter that the '799 patent requires the use of a generic computer rather than pen and paper. Indeed, the Federal Circuit routinely rejects "do it on a computer" patents that seek "to automate 'pen and paper methodologies' to conserve human resources and minimize errors." *Univ. of Fla. Rsch. Found., Inc. v. Gen. Elec. Co.*, 916 F.3d 1363, 1367 (Fed. Cir. 2019); *accord*, *e.g.*, *In re Stanford*, 991 F.3d at 1250; *Accenture Glob. Servs., GmbH v. Guidewire Software, Inc.*, 728 F.3d 1336, 1339, 1342 (Fed. Cir. 2013). As the Federal Circuit has held, the mere application of a generic computer is not a technological improvement. *See Intell. Ventures I LLC v. Symantec Corp.*, 838 F.3d 1307, 1318 (Fed. Cir. 2016).

Nor does it matter that using a computer facilitates a data comparison that would be complex or time-consuming to perform mentally. The Federal Circuit has consistently held that an abstract idea does not become patentable simply because a computer improves the speed, accuracy, or volume of information processing, or because the computer permits a comparison that would be impossibly time-consuming to perform by hand. *See Bancorp Servs., L.L.C. v. Sun Life Assur. Co. of Canada (U.S.)*, 687 F.3d 1266, 1278 (Fed. Cir. 2012); *see also BroadSoft, Inc. v. CallWave Commc'ns, LLC*, 282 F. Supp. 3d 771, 781 (D. Del. 2017), *aff'd*, 739 F. App'x 985 (Fed. Cir. 2018) (quoting *Cyberfone Sys., LLC v. CNN Interactive Group, Inc.*, 558 F. Appx. 988, 992 (Fed. Cir. 2014) ("[T]he category of patent-ineligible abstract ideas is not limited to methods that can be performed in the human mind")).[3]

[3] For this reason, the Examiner's Notice of Allowance (Ex. A), which cited the added step of aligning the contig to a reference genome, and noted that the "added step is not practical to be performed in the mind because of the large size of the reference genomes," and consequently "does not recite a mental process . . . or any other grouping of an abstract idea," was legally erroneous.

Invitae alleges that the claims of the '799 patent are not directed to an abstract idea "but are rather directed to a concrete technique that … improves upon and realizes the full potential of … DNA sequencing technology[,]" and "[i]n particular," the sequencing platform sold commercially by Illumina. D.I. 1 at ¶ 16. But nothing in the Complaint, the specification, or the claims themselves recite any specific improvement upon any DNA sequencing technology, much less Illumina's sequencing platform. Rather, the specification and the claims recite sequencing merely as a conventional source of the data on which the claimed algorithmic steps are performed. A complaint does not state a valid claim "if it tenders 'naked assertion[s]' devoid of 'further factual enhancement.'" *Iqbal*, 556 U.S. at 678 (quoting *Twombly*, 550 U.S. at 556).

Invitae also alleges that comparing the "reads" to the "contigs" solves a prior-art trade-off between sensitivity to different types of mutations (omissions/deletions versus substitutions). *See*, *e.g.*, *id.* at ¶¶ 11, 15, 16, 18. But even if these conclusory allegations were taken as true, the Federal Circuit in *Stanford* rejected the same argument Invitae makes here, holding that "improvement in computational accuracy … does not qualify as an improvement to a technological process; rather, it is merely an enhancement to the abstract [idea] itself." *Stanford*, 991 F.3d at 1251.[4] Any such improvement that the '799 patent supposedly made is thus still an abstract idea. *See id.*

[4] Plaintiff suggests that the improved data comparison bears on the *Alice* Step Two analysis. *See* Compl. ¶ 18. The Federal Circuit, however, examines improvement of a technological process under *Alice* Step One. *See Stanford*, 991 F.3d at 1250-51 ("We have also examined, at *Alice* step one, whether the claimed advance alleged in the written description demonstrates an improvement of a technological process or merely enhances an ineligible concept."); *see also Athena Diagnostics, Inc. v. Mayo Collaborative Servs., LLC*, 915 F.3d 743, 750 (Fed. Cir. 2019) ("To determine whether a claim is directed to an ineligible concept, we have frequently considered whether the claimed advance improves upon a technological process or merely an ineligible concept, based on both the written description and the claims.").

B. *Alice* Step Two: The '799 Patent Claims Lack an Inventive Concept Because They Recite Only Well-Known and Conventional Steps

At *Alice* step two, the Court determines whether the claims contain any other limitations—individually and as an ordered combination and apart from those embodying the ineligible subject matter itself—that establish an inventive concept that transforms the abstract idea into patent eligible subject matter. *Alice*, 573 U.S. at 222; *see also Mayo Collaborative Servs. v. Prometheus Labs, Inc.*, 566 U.S. 66, 78 (2012). "To save a patent at step two, an inventive concept must be evident in the claims." *RecogniCorp*, 855 F.3d at 1327. Well understood, routine, and conventional elements do not amount to an inventive concept and cannot satisfy step two. *Alice*, 573 U.S. at 222, 225. Nor can the abstract idea itself supply the requisite inventive concept. *See Cellspin Soft, Inc. v. Fitbit, Inc.*, 927 F.3d 1306, 1316 (Fed. Cir. 2019) ("If a claim's only 'inventive concept' is the application of an abstract idea using conventional and well-understood techniques, the claim has not been transformed into a patent-eligible application of an abstract idea.") (quoting *BSG Tech LLC v. Buyseasons, Inc.*, 899 F.3d 1281, 1290-91 (Fed. Cir. 2018)); *Genetic Techs.*, 818 F.3d at 1376 ("The inventive concept necessary at step two of the *Mayo/Alice* analysis cannot be furnished by the unpatentable law of nature (or natural phenomenon or abstract idea) itself.").

"In a situation where the specification admits the additional claim elements are well-understood, routine, and conventional, it will be difficult, if not impossible, for a patentee to show a genuine dispute." *Aatrix Software, Inc. v. Green Shades Software, Inc.*, 890 F.3d 1354, 1356 (Fed. Cir. 2018) (Moore, J.) (concurring in denial of rehearing *en banc*); *see also Citrix Sys.*, 363 F. Supp. 3d at 520.

Here, the '799 patent specification leaves no room for dispute. Aside from the algorithmic steps of assembling, aligning, and combining data, the only limitations left are "obtaining" a sample comprising DNA and "sequencing" the DNA to generate the sequence reads. But the

patent admits—and there is no dispute arising from the allegations in the Complaint —that both of those steps were conventional and well known in the art. The patent devotes over a column of text to recycling the prior art about how to obtain a DNA sample, *see, e.g.*, D.I. 1-1, Ex. 1 at 5:60-63; 6:16-18, 6:30-36, and does not purport to improve on the prior art in this regard. Likewise, the patent states that DNA-sequencing can be accomplished "by any method known in the art," *id.* at 9:56, and recounts the many established DNA-sequencing techniques that could be employed to practice the claims, *see*, *e.g.*, *id.* at 9:56-67; 10:5-12:23, while not purporting to have advanced that prior art at all. These steps of obtaining and sequencing a DNA sample, then, are "insignificant pre-solution activity" that is "not sufficient to transform an otherwise patent-ineligible abstract idea into patent-eligible subject matter." *Ultramercial, Inc. v. Hulu, LLC*, 772 F.3d 709, 715 (Fed. Cir. 2014) (internal quotation marks omitted); *accord In re TLI Commc'ns LLC Pat. Litig.*, 823 F.3d 607, 614 (Fed. Cir. 2016).

Invitae cites to two paragraphs in the patent as supporting an inventive concept. D.I. 1 at ¶ 18 (citing D.I. 1-1, Ex. 1 at 2:53-58, 4:38-57). But as discussed above, the cited paragraphs only confirm the abstract nature of the invention. The law is clear that an abstract idea itself cannot be the additional "inventive step" that makes a claim patent-eligible at step two. *See Cellspin Soft*, 927 F.3d at 1316; *BSG*, 899 F.3d at 1290-91; *Genetic Techs.*, 818 F.3d at 1376.

C. The Dependent Claims Fare No Better Under *Alice*

Substantially similar claims directed to the same abstract idea can be considered together for subject-matter eligibility. *Content Extraction & Transmission LLC v. Wells Fargo Bank*, 776 F.3d 1343, 1348 (Fed. Cir. 2014); *see also FiscalNote, Inc. v. Quorum Analytics Inc.*, C.A. No. 20-1736-LPS (D. Del. June 25, 2021), Tr. at 136 (Ex. B) (addressing only representative claims where additional claims were "substantially similar and linked to the same abstract idea"). Natera

has focused this motion on claim 1 because the Complaint itself alleges that claim 1 is "[r]epresentative." D.I. 1 at ¶ 15.

For completeness, however, Natera notes that the dependent claims are also ineligible for patenting. The dependent claims all proceed from the same abstract idea: an algorithmic method of manipulating and combining genetic sequence data using an intermediate data set. They all recite the same well understood, routine, conventional steps of obtaining a DNA sample and sequencing it. And they all require a generic computer to perform the algorithmic method. Some of them specify a particular prior-art DNA-sequencing technique (claims 2-5, 13, 14) and/or the math or algorithm, which is itself abstract (claims 3, 4, 6, 7, 15, 16), or require the identification of one or more naturally occurring mutations based on the math work (claims 8-12). But none of them adds an inventive concept. Limiting the application of an abstract idea to specific conventional, routine operations does not make the abstract idea patent eligible. *BSG Tech*, 899 F.3d at 1287 ("[A] claim is not patent eligible merely because it applies an abstract idea in a narrow way."). For the same reasons why claim 1 fails, the dependent claims fail under Section 101 too.

VI. CONCLUSION

The inventors of the '799 patent claim to have discovered that information from DNA datasets—reads and contigs—can be compared and combined using existing, prior-art computers and software into a new form that is better than prior-art analyses. That is not a patentable invention. It is, at best, an improved abstract idea. As the undisputed facts set forth in the intrinsic record shows, nothing about the patent claims adds an inventive concept sufficient to save the claims. Natera respectfully requests that the Court dismiss Invitae's Complaint with prejudice.

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June 30, 2021

CERTIFICATE OF SERVICE

I hereby certify that on June 30, 2021, I caused the foregoing to be electronically filed with the Clerk of the Court using CM/ECF, which will send notification of such filing to all registered participants.

I further certify that I caused copies of the foregoing document to be served on June 30, 2021, upon the following in the manner indicated:

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